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Reviewer: Keisha Douglas

Timestamp: [year=2008; month=11; day=18; hr=18; min=38; sec=30; ms=789;
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Application No: 10590464

Version No: 1.0

Input Set:

Output Set:

Started: 2008-10-21 19:04:04.576

Finished: 2008-10-21 19:04:06.187

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 611 ms

Total Warnings: 25

Total Errors: 0

No. of SeqIDs Defined: 29

Actual SeqID Count: 29

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W 213	Artificial or Unknown found in <213> in SEQ ID (9)
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W 213	Artificial or Unknown found in <213> in SEQ ID (23)
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Input Set:

Output Set:

Started: 2008-10-21 19:04:04.576
Finished: 2008-10-21 19:04:06.187
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 611 ms
Total Warnings: 25
Total Errors: 0
No. of SeqIDs Defined: 29
Actual SeqID Count: 29

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

<110> Kihara Memorial Yokohama Foundation for the Advancement of Life Sciences
City of Yokohama

<120> TRF2 DNA-binding domain mutant proteins, telomeric DNA mutants, and use of a structure of a complex between a TRF2 DNA binding domain and a double-stranded DNA molecule

<130> FP-047PCT

<140> 10590464

<141> 2008-10-21

<150> JP P2004-046238

<151> 2004-02-23

<160> 29

<170> PatentIn version 3.1

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<211> 189

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(189)

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atg att aag gat cgc tgg cgg acc atg aaa aga ctt ggc atg aac 189
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<211> 63

<212> PRT

<213> Homo sapiens

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Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn	
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Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val	
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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac	96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn	
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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac	96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn	
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Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val	
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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac	96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn	
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tgg gct gcc att tct aaa aat tac cca ttt gtt aac cga aca gct gtg	144
Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val	
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atg att aag gat cgc tgg cgg acc atg aaa aag ctt ggc atg aac	189
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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac	96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn	
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tgg tct gcc att tct aaa aat tac cca ttt gtt aac cga aca tct gtg	144
Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val	
35 40 45	

atg att aag gat cgc tgg cgg acc atg aaa aag ctt ggc atg aac	189
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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac	96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn	
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tgg tct gcc att tct aaa aat tac cca ttt gtt aac cga aca tct gtg	144
Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val	
35 40 45	

atg att aag gat cgc tgg cgg acc atg aaa aga ctt ggc atg aac	189
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<220>
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agg cgg gcg tcc cgc agt agc ggg cgg gcc cgg cgg ggg cgc cac gag	96
Arg Arg Ala Ser Arg Ser Ser Gly Arg Ala Arg Arg Gly Arg His Glu	
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ccg ggg ctg ggg ggc ccg gcg gag cgc ggc gcg ggg gag gca cgg ctg	144
Pro Gly Leu Gly Gly Pro Ala Glu Arg Gly Ala Gly Glu Ala Arg Leu	
35 40 45	
gaa gag gca gtc aat cgc tgg gtg ctc aag ttc tac ttc cac gag gcg	192
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50 55 60	
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Leu Arg Ala Phe Arg Gly Ser Arg Tyr Gly Asp Phe Arg Gln Ile Arg	
65 70 75 80	
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Asp Ile Met Gln Ala Leu Leu Val Arg Pro Leu Gly Lys Glu His Thr	
85 90 95	
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Val Ser Arg Leu Leu Arg Val Met Gln Cys Leu Ser Arg Ile Glu Glu	
100 105 110	
ggg gaa aat tta gac tgt tcc ttt gat atg gag gct gag ctc aca cca	384
Gly Glu Asn Leu Asp Cys Ser Phe Asp Met Glu Ala Glu Leu Thr Pro	
115 120 125	

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130 135 140	
ctg aca gaa gca gtg gtc gaa tcc agt aga aaa ctg gtc aag gaa gct	480
Leu Thr Glu Ala Val Val Glu Ser Ser Arg Lys Leu Val Lys Glu Ala	
145 150 155 160	
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Ala Val Ile Ile Cys Ile Lys Asn Lys Glu Phe Glu Lys Ala Ser Lys	
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Asn Asp Leu Leu Asn Ile Ile Arg Glu Lys Asn Leu Ala His Pro Val	
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Leu Glu Ser His Leu Asp Asp Ala Glu Pro Tyr Leu Leu Thr Met Ala	
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Asp Lys Gln Pro Ala Pro Gly Pro Val Glu Lys Pro Pro Arg Glu Pro	
260 265 270	
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Ala Arg Gln Leu Arg Asn Pro Pro Thr Thr Ile Gly Met Met Thr Leu	
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Lys Ala Ala Phe Lys Thr Leu Ser Gly Ala Gln Asp Ser Glu Ala Ala	
290 295 300	
ttt gca aaa ctg gac cag aag gat ctg gtt ctt cct act caa gct ctc	960
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325 330 335	
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